

# **Microarray Analysis Reveals Distinct Gene Expression Profiles among Different Histologic Types of Endometrial Cancer**

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## **Abstract**

**Previous studies of oncogene and tumor suppressor gene alterations have suggested that differences exist in the molecular pathogenesis of the various histological types of endometrial cancer. To elucidate further the molecular events involved in endometrial carcinogenesis, we examined global expression patterns of 16 nonendometrioid cancers (13 serous papillary and 3 clear cell), 19 endometrioid cancers, and 7 age-matched normal endometria using cDNA microarrays. Unsupervised analysis of gene expression identified 191 genes that exhibited >2-fold differences ( $P < 0.001$ ) between the histological groups. Many genes were similarly dysregulated in both nonendometrioid and endometrioid cancers relative to normal endometria. Gene expression differences in only 24 transcripts could distinguish serous from endometrioid cancers, the two most common subgroups. These data provide the basis for investigation of previously unrecognized novel pathways involved in the development of endometrial cancers.**